

IAP13 Rec'd PCT/PTO 12 DEC 2005

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SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

<120> MODIFIED FIBER PROTEINS FOR EFFICIENT
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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro	
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Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser	
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cta	cgc	gtc	tcc	gaa	cct	ttg	gac	acc	tcc	cac	ggc	atg	ctt	gcg	ctt	192
Leu	Arg	Val	Ser	Glu	Pro	Leu	Asp	Thr	Ser	His	Gly	Met	Leu	Ala	Leu	
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Gln	Asn	Val	Thr	Thr	Val	Thr	Gln	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	
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Ile	Ser	Leu	Asp	Thr	Ser	Ala	Pro	Leu	Thr	Ile	Thr	Ser	Gly	Ala	Leu	
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Thr	Val	Ala	Thr	Thr	Ala	Pro	Leu	Ile	Val	Thr	Ser	Gly	Ala	Leu	Ser	
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ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr	260	265	270	816
cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro	275	280	285	864
ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly	290	295	300	912
cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser	305	310	315	960
ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile	325	330	335	1008
aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro	340	345	350	1056
gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn	355	360	365	1104
gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp	370	375	380	1152
aac tca ggg gcc att aca ata gga aac aaa aat gat gac aaa ctt acc Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr	385	390	395	1200
ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp	405	410	415	1248
aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val	420	425	430	1296
cta gct act gta gct gct ttg gct gta tct gga gat ctt tca tcc atg Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met	435	440	445	1344
aca ggc acc gtt gca agt gtt agt ata ttc ctt aga ttt gac caa aac Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn	450	455	460	1392
ggt gtt cta atg gag aac tcc tca ctt aaa aaa cat tac tgg aac ttt Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe	465	470	475	1440
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Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
      500      505      510

aaa aat aac att gtc agt caa gtt tac ttg cat ggt gat aaa act aaa 1584
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
      515      520      525

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Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
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tcc tac att gcc cag gaa taa 1749
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<213> Adenovirus serotype 2 fiber

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      35      40      45
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
      50      55      60
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
      65      70      75      80
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
      85      90      95
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
      100      105      110
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
      115      120      125
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
      130      135      140
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
      145      150      155      160
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
      165      170      175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
      180      185      190
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser

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		195					200				205				
Gly	Pro	Leu	Gln	Val	Ala	Gln	Asn	Ser	Asp	Thr	Leu	Thr	Val	Val	Thr
	210					215					220				
Gly	Pro	Gly	Val	Thr	Val	Glu	Gln	Asn	Ser	Leu	Arg	Thr	Lys	Val	Ala
225					230					235					240
Gly	Ala	Ile	Gly	Tyr	Asp	Ser	Ser	Asn	Asn	Met	Glu	Ile	Lys	Thr	Gly
				245					250					255	
Gly	Gly	Met	Arg	Ile	Asn	Asn	Asn	Leu	Leu	Ile	Leu	Asp	Val	Asp	Tyr
			260					265					270		
Pro	Phe	Asp	Ala	Gln	Thr	Lys	Leu	Arg	Leu	Lys	Leu	Gly	Gln	Gly	Pro
		275					280					285			
Leu	Tyr	Ile	Asn	Ala	Ser	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	Arg	Gly
	290					295					300				
Leu	Tyr	Leu	Phe	Asn	Ala	Ser	Asn	Asn	Thr	Lys	Lys	Leu	Glu	Val	Ser
305					310					315					320
Ile	Lys	Lys	Ser	Ser	Gly	Leu	Asn	Phe	Asp	Asn	Thr	Ala	Ile	Ala	Ile
				325					330					335	
Asn	Ala	Gly	Lys	Gly	Leu	Glu	Phe	Asp	Thr	Asn	Thr	Ser	Glu	Ser	Pro
			340					345					350		
Asp	Ile	Asn	Pro	Ile	Lys	Thr	Lys	Ile	Gly	Ser	Gly	Ile	Asp	Tyr	Asn
		355					360					365			
Glu	Asn	Gly	Ala	Met	Ile	Thr	Lys	Leu	Gly	Ala	Gly	Leu	Ser	Phe	Asp
	370					375					380				
Asn	Ser	Gly	Ala	Ile	Thr	Ile	Gly	Asn	Lys	Asn	Asp	Asp	Lys	Leu	Thr
385					390					395					400
Leu	Trp	Thr	Thr	Pro	Asp	Pro	Ser	Pro	Asn	Cys	Arg	Ile	His	Ser	Asp
				405					410					415	
Asn	Asp	Cys	Lys	Phe	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Val
			420					425					430		
Leu	Ala	Thr	Val	Ala	Ala	Leu	Ala	Val	Ser	Gly	Asp	Leu	Ser	Ser	Met
		435					440					445			
Thr	Gly	Thr	Val	Ala	Ser	Val	Ser	Ile	Phe	Leu	Arg	Phe	Asp	Gln	Asn
	450					455					460				
Gly	Val	Leu	Met	Glu	Asn	Ser	Ser	Leu	Lys	Lys	His	Tyr	Trp	Asn	Phe
465					470					475					480
Arg	Asn	Gly	Asn	Ser	Thr	Asn	Ala	Asn	Pro	Tyr	Thr	Asn	Ala	Val	Gly
				485					490					495	
Phe	Met	Pro	Asn	Leu	Leu	Ala	Tyr	Pro	Lys	Thr	Gln	Ser	Gln	Thr	Ala
			500					505					510		
Lys	Asn	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	His	Gly	Asp	Lys	Thr	Lys
		515					520					525			
Pro	Met	Ile	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Ser	Glu	Ser	Thr	Glu
	530														

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<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber
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<220>
<221> CDS
<222> (1) ... (1746)
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<400> 34

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atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca	48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc	192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768

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Gly	Ala	Leu	Gly	Phe 245	Asp	Ser	Gln	Gly	Asn 250	Met	Gln	Leu	Asn	Val 255	Ala		
gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	ggt	816	
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn 265	Arg	Arg	Leu	Ile	Leu	Asp	Val		
agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	cta	gga	cag	864	
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn 280	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln		
ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	aac	tac	aac	912	
Gly	Pro	Leu	Phe	Ile	Asn	Ser 295	Ala	His	Asn	Leu	Asp 300	Ile	Asn	Tyr	Asn		
aaa	ggc	ctt	tac	ttg	ttt	aca	gct	tca	aac	aat	tcc	aaa	aag	ctt	gag	960	
Lys	Gly	Leu	Tyr	Leu	Phe 310	Thr	Ala	Ser	Asn	Met 315	Ser	Lys	Lys	Leu	Glu 320		
gtt	aac	cta	agc	act	gcc	aag	ggg	ttg	atg	ttt	gac	gct	aca	gcc	ata	1008	
Val	Asn	Leu	Ser	Thr 325	Ala	Lys	Gly	Leu	Met 330	Phe	Asp	Ala	Thr	Ala	Ile 335		
gcc	att	aat	gca	gga	gat	ggg	ctt	gaa	ttt	ggt	tca	cct	aat	gca	cca	1056	
Ala	Ile	Asn	Ala 340	Gly	Asp	Gly	Leu	Glu 345	Phe	Gly	Ser	Pro	Asn	Ala	Pro 350		
aac	aca	aat	ccc	ctc	aaa	aca	aaa	att	ggc	cat	ggc	cta	gaa	ttt	gat	1104	
Asn	Thr	Asn	Pro	Leu	Lys	Thr 360	Lys	Ile	Gly	His	Gly	Leu	Glu	Phe	Asp 365		
tca	aac	aag	gct	atg	gtt	cct	aaa	cta	gga	act	ggc	ctt	agt	ttt	gac	1152	
Ser	Asn	Lys	Ala	Met	Val	Pro 375	Lys	Leu	Gly	Thr	Gly 380	Leu	Ser	Phe	Asp 385		
agc	aca	ggt	gcc	att	aca	gta	gga	aac	aaa	aat	aat	gat	aag	cta	act	1200	
Ser	Thr	Gly	Ala	Ile	Thr 390	Val	Gly	Asn	Lys	Asn 395	Asn	Asp	Lys	Leu	Thr 400		
ttg	tgg	acc	aca	cca	gct	cca	tct	cct	aac	tgt	aga	cta	aat	gca	gag	1248	
Leu	Trp	Thr	Thr 405	Pro	Ala	Pro	Ser	Pro	Asn 410	Cys	Arg	Leu	Asn	Ala	Glu 415		
aaa	gat	gct	aaa	ctc	act	ttg	gtc	tta	aca	aaa	tgt	ggc	agt	caa	ata	1296	
Lys	Asp	Ala	Lys 420	Leu	Thr	Leu	Val	Leu	Thr 425	Lys	Cys	Gly	Ser	Gln	Ile 430		
ctt	gct	aca	gtt	tca	gtt	ttg	gct	gtt	aaa	ggc	agt	ttg	gct	cca	ata	1344	
Leu	Ala	Thr	Val 435	Ser	Val	Leu	Ala 440	Val	Lys	Gly	Ser	Leu	Ala	Pro	Ile 445		
tct	gga	aca	gtt	caa	agt	gct	cat	ctt	att	ata	aga	ttt	gac	gaa	aat	1392	
Ser	Gly	Thr	Val 450	Gln	Ser	Ala 455	His	Leu	Ile	Ile	Arg 460	Phe	Asp	Glu	Asn 465		
gga	gtg	cta	cta	aac	aat	tcc	ttc	ctg	gac	cca	gaa	tat	tgg	aac	ttt	1440	
Gly	Val	Leu	Leu	Asn	Asn 470	Ser	Phe	Leu	Asp 475	Pro	Glu	Tyr	Trp	Asn	Phe 480		
aga	aat	gga	gat	ctt	act	gaa	ggc	aca	gcc	tat	aca	aac	gct	gtt	gga	1488	
Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly		

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485										490					495					
ttt	atg	cct	aac	cta	tca	gct	tat	cca	aaa	tct	cac	ggg	aaa	act	gcc	1536				
Phe	Met	Pro	Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala					
			500					505					510							
aaa	agt	aac	att	gtc	agt	caa	gtt	tac	tta	aac	gga	gac	aaa	act	aaa	1584				
Lys	Ser	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys					
		515					520					525								
cct	gta	aca	cta	acc	att	aca	cta	aac	ggg	aca	cag	gaa	aca	gga	gac	1632				
Pro	Val	Thr	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp					
		530				535					540									
aca	act	cca	agt	gca	tac	tct	atg	tca	ttt	tca	tgg	gac	tgg	tct	ggc	1680				
Thr	Thr	Pro	Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly					
545				550				555							560					
cac	aac	tac	att	aat	gaa	ata	ttt	gcc	aca	tcc	tct	tac	act	ttt	tca	1728				
His	Asn	Tyr	Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser					
			565					570						575						
tac	att	gcc	caa	gaa	taa											1746				
Tyr	Ile	Ala	Gln	Glu	*															
			580																	

<210> 35

<211> 581

<212> PRT

<213> Adenovirus serotype 5 fiber

<400> 35

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro
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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro
			20					25					30		
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser
		35				40						45			
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu
	50					55					60				
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser
65					70					75					80
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn
			85						90					95	
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu
		100						105					110		
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr
		115				120						125			
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile
		130				135					140				
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln
145					150					155					160
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr
			165						170					175	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu
		180						185					190		
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly
		195					200					205			
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr
		210				215					220				

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Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
 450 455 460
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
 485 490 495
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
 530 535 540
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 565 570 575
 Tyr Ile Ala Gln Glu
 580

<210> 36
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 37 fiber

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 36
 atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc 48
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15

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tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt	96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc	144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag	192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct	240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat	288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga	336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat	384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa	432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta	480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca	528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca	576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg	624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
195 200 205	
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att	672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile	
210 215 220	
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa	720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys	
225 230 235 240	
ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt	768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu	
245 250 255	

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tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tgc aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
340 345 350	
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *	
355 360 365	

<210> 37

<211> 365

<212> PRT

<213> Adenovirus serotype 37 fiber

<400> 37

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	

Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile
210	210					215					220				
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Lys
225					230					235					240
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu
				245					250					255	
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly
				260				265					270		
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro
				275			280					285			
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg
				290		295					300				
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro
305					310					315					320
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser
				325					330					335	
Ile	Thr	Phe	Asn	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe
				340				345					350		
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu			
		355					360					365			

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<210> 38
<211> 1098
<212> DNA
<213> Adenovirus serotype 19p fiber
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<220>
<221> CDS
<222> (1) ... (1098)
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<400>	38																
atg	tca	aag	agg	ctc	cgg	gtg	gaa	gat	gac	ttc	aac	ccc	gtc	tac	ccc		48
Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro		
1				5					10					15			
tat	ggc	tac	gcg	cgg	aat	cag	aat	atc	ccc	ttc	ctc	act	ccc	ccc	ttt		96
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe		
			20					25					30				
gtc	tcc	tcc	gat	gga	ttc	aaa	aac	ttc	ccc	cct	ggg	gta	ctg	tca	ctc		144
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu		
			35				40					45					
aaa	ctg	gct	gat	cca	atc	acc	att	acc	aat	ggg	gat	gta	tcc	ctc	aag		192
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys		
	50					55					60						
gtg	gga	ggg	ggg	ctc	act	ttg	caa	gat	gga	agc	cta	act	gta	aac	cct		240
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro		
65					70					75					80		
aag	gct	cca	ctg	caa	gtt	act	act	gat	aaa	aaa	ctt	gag	ctt	gca	tat		288
Lys	Ala	Pro	Leu	Gln	Val	Thr	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr		
				85					90					95			
gat	aat	cca	ttt	gaa	tgt	agt	gct	aat	aaa	ttt	agt	tta	aaa	gta	gga		336
Asp	Asn	Pro	Phe	Glu	Cys	Ser	Ala	Asn	Lys	Phe	Ser	Leu	Lys	Val	Gly		
			100					105					110				

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cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat	384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa	432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta	480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca	528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca	576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg	624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
195 200 205	
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att	672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile	
210 215 220	
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa	720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu	
225 230 235 240	
ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt	768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu	
245 250 255	
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
340 345 350	
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098

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Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *

355 360 365

<210> 39

<211> 365

<212> PRT

<213> Adenovirus serotype 19p fiber

<400> 39

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1 5 10 15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Phe
20 25 30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
35 40 45
Lys Leu Ala Asp Pro Ile Thr Thr Asn Gly Asp Val Ser Leu Lys
50 55 60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65 70 75 80
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
85 90 95
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
100 105 110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
115 120 125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
130 135 140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145 150 155 160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
165 170 175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
180 185 190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
195 200 205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
210 215 220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225 230 235 240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
245 250 255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
260 265 270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
275 280 285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
290 295 300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305 310 315 320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
325 330 335
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
340 345 350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
355 360 365

<210> 40

<211> 1228

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<212> DNA

<213> Adenovirus serotype 9 fiber

<220>

<221> CDS

<222> (50)...(1138)

<400> 40

aagggatgac aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58
 Met Ser Lys
 1

agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac 106
 Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
 5 10 15

gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc 154
 Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
 20 25 30 35

gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct 202
 Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
 40 45 50

gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg 250
 Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
 55 60 65

ggg ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat 298
 Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
 70 75 80

cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct 346
 Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
 85 90 95

cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc 394
 Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
 100 105 110 115

ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat 442
 Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
 120 125 130

act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat 490
 Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
 135 140 145

aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca 538
 Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
 150 155 160

ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag 586
 Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
 165 170 175

cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat 634
 Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
 180 185 190 195

cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt 682

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Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	
				200					205					210		
caa	ata	ttg	gct	aat	gtg	tca	tta	att	gtc	gta	gat	ggt	aag	tac	aaa	730
Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Asp	Gly	Lys	Tyr	Lys	
			215					220					225			
att	atc	aat	aac	aat	act	caa	cca	gct	ctc	aaa	gga	ttt	acc	att	aaa	778
Ile	Ile	Asn	Asn	Asn	Thr	Gln	Pro	Ala	Leu	Lys	Gly	Phe	Thr	Ile	Lys	
		230					235					240				
tta	ttg	ttt	gat	gaa	aat	gga	gta	ctt	atg	gaa	tct	tca	aat	ctt	ggt	826
Leu	Leu	Phe	Asp	Glu	Asn	Gly	Val	Leu	Met	Glu	Ser	Ser	Asn	Leu	Gly	
	245					250					255					
aaa	tca	tat	tgg	aac	ttt	aga	aat	gaa	aat	tca	att	atg	tca	aca	gct	874
Lys	Ser	Tyr	Trp	Asn	Phe	Arg	Asn	Glu	Asn	Ser	Ile	Met	Ser	Thr	Ala	
	260				265					270					275	
tat	gaa	aaa	gct	att	gga	ttc	atg	cct	aat	ttg	gta	gcc	tat	cca	aaa	922
Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	Tyr	Pro	Lys	
				280					285					290		
cct	acc	gct	ggc	tct	aaa	aaa	tat	gca	aga	gat	ata	gtt	tat	gga	aac	970
Pro	Thr	Ala	Gly	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val	Tyr	Gly	Asn	
			295					300					305			
atc	tac	ctt	ggt	gga	aag	cca	gat	caa	cca	gta	acc	att	aaa	act	acc	1018
Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	Val	Thr	Ile	Lys	Thr	Thr	
		310					315					320				
ttt	aat	cag	gaa	act	gga	tgt	gaa	tat	tct	atc	aca	ttt	gat	ttt	agt	1066
Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asp	Phe	Ser	
	325					330					335					
tgg	gcc	aag	act	tat	gta	aat	gtt	gaa	ttt	gaa	aca	acc	tct	ttt	acc	1114
Trp	Ala	Lys	Thr	Tyr	Val	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr	
	340				345					350					355	
ttt	tcc	tat	atc	gcc	caa	gaa	tga	aagaccaata	aacgtgtttt	tcattttcaaa						1168
Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*									
				360												
atttttcatgt	atctttattg	attttttacac	cagcacgggt	agtcagtctc	ccaccaccag											1228

<210> 41

<211> 362

<212> PRT

<213> Adenovirus serotype 9 fiber

<400> 41

Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro	
1				5					10					15		
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe	
			20					25					30			
Val	Ser	Ser	Asp	Gly	Phe	Gln	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu	
		35					40					45				
Lys	Leu	Ala	Asp	Pro	Ile	Ala	Ile	Val	Asn	Gly	Asn	Val	Ser	Leu	Lys	
	50					55					60					
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Thr	Gly	Lys	Leu	Thr	Val	

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65					70					75				80	
Asn	Ala	Asp	Pro	Pro	Leu	Gln	Leu	Thr	Asn	Asn	Lys	Leu	Gly	Ile	Ala
				85					90					95	
Leu	Asp	Ala	Pro	Phe	Asp	Val	Ile	Asp	Asn	Lys	Leu	Thr	Leu	Leu	Ala
			100					105					110		
Gly	His	Gly	Leu	Ser	Ile	Ile	Thr	Lys	Glu	Thr	Ser	Thr	Leu	Pro	Gly
	115						120					125			
Leu	Arg	Asn	Thr	Leu	Val	Val	Leu	Thr	Gly	Lys	Gly	Ile	Gly	Thr	Glu
	130				135						140				
Ser	Thr	Asp	Asn	Gly	Gly	Thr	Val	Cys	Val	Arg	Val	Gly	Glu	Gly	Gly
145				150						155					160
Gly	Leu	Ser	Phe	Asn	Asn	Asp	Gly	Asp	Leu	Val	Ala	Phe	Asn	Lys	Lys
			165					170						175	
Glu	Asp	Lys	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr	Ser	Pro	Asn	Cys
			180					185					190		
Lys	Ile	Asp	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys
	195						200					205			
Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Asp	Gly
	210					215					220				
Lys	Tyr	Lys	Ile	Ile	Asn	Asn	Asn	Thr	Gln	Pro	Ala	Leu	Lys	Gly	Phe
225				230						235					240
Thr	Ile	Lys	Leu	Leu	Phe	Asp	Glu	Asn	Gly	Val	Leu	Met	Glu	Ser	Ser
			245					250					255		
Asn	Leu	Gly	Lys	Ser	Tyr	Trp	Asn	Phe	Arg	Asn	Glu	Asn	Ser	Ile	Met
			260					265					270		
Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala
	275					280					285				
Tyr	Pro	Lys	Pro	Thr	Ala	Gly	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val
	290				295						300				
Tyr	Gly	Asn	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	Val	Thr	Ile
305				310						315					320
Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe
			325					330					335		
Asp	Phe	Ser	Trp	Ala	Lys	Thr	Tyr	Val	Asn	Val	Glu	Phe	Glu	Thr	Thr
			340					345					350		
Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu						
			355				360								

<210> 42
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad2 third repeat

<400> 42
 Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
 1 5 10 15
 Lys Thr Lys Ser
 20

<210> 43
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5 third repeat

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<400> 43

Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
 1 5 10 15
 Lys Thr Lys Ser
 20

<210> 44

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Repeat motif

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ser

<400> 44

Thr Thr Val Xaa
 1

<210> 45

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Repeat Consensus Sequence

<221> VARIANT

<222> 3,5,7,13

<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT

<222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 10

<223> Xaa = Pro or Gly

<400> 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

<210> 46

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad2 21st repeat

<400> 46

Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
 1 5 10 15

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<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1 5

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5Ds fiber

<221> CDS
<222> (13)...(1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G

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<400> 50

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atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
      Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
        1             5             10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
      15             20             25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
      30             35             40             45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
      50             55             60

ctt gcg ctg aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
      65             70             75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
      80             85             90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
      95             100             105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
      110             115             120             125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
      130             135             140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
      145             150             155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat 531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
      160             165             170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt 579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
      175             180             185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa 627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys
      190             195             200             205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc 675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
      210             215             220             225

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata 723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
      225             230             235

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aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca 771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro
      240      245      250

gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat 819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr
      255      260      265

aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct 867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser
      270      275      280      285

cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac 915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn
      290      295      300

gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca 963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr
      305      310      315

cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca 1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser
      320      325      330

tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc 1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser
      335      340      345

tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa 1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *
      350      355

gggcgaattc cagcacantg gcggccggtta ttagtggatc cgagntcatg ca 1164

<210> 51
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5deltas

<400> 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1      5      10      15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20      25      30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35      40      45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50      55      60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65      70      75      80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys
85      90      95
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr
100      105      110
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn
115      120      125
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu
130      135      140

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Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
 145 150 155 160
 Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
 165 170 175
 Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
 180 185 190
 Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
 195 200 205
 Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
 210 215 220
 Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
 225 230 235 240
 Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
 245 250 255
 Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
 260 265 270
 Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
 275 280 285
 Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
 290 295 300
 Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
 305 310 315 320
 Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
 325 330 335
 Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
 340 345 350
 Phe Ser Tyr Ile Ala Gln Glu
 355

<210> 52
 <211> 1920
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37k fiber

<221> CDS
 <222> (13)...(1755)

<221> misc feature
 <222> 1867, 1875
 <223> n = A,T,C or G

<400> 52
 gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10
 gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25
 act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45
 gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

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ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac	243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn	
65 70 75	
ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc	291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr	
80 85 90	
aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca	339
Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser	
95 100 105	
gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac	387
Glu Ala Leu Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn	
110 115 120 125	
aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa	435
Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys	
130 135 140	
ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta	483
Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu	
145 150 155	
gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt	531
Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu	
160 165 170	
act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc	579
Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly	
175 180 185	
att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta	627
Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu	
190 195 200 205	
aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc	675
Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr	
210 215 220	
gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act	723
Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr	
225 230 235	
aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt	771
Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu	
240 245 250	
aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata	819
Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile	
255 260 265	
ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga	867
Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg	
270 275 280 285	
cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att	915
Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile	
290 295 300	

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aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa	963
Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys	
305 310 315	
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct	1011
Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala	
320 325 330	
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct	1059
Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro	
335 340 345	
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta	1107
Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu	
350 355 360 365	
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt	1155
Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu	
370 375 380	
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat	1203
Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp	
385 390 395	
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att	1251
Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile	
400 405 410	
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga	1299
Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly	
415 420 425	
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac	1347
Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr	
430 435 440 445	
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att	1395
His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile	
450 455 460	
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt	1443
Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu	
465 470 475	
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca	1491
Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr	
480 485 490	
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca	1539
Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro	
495 500 505	
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act	1587
Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr	
510 515 520 525	
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc	1635
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr	
530 535 540	
ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683

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Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asn	Phe	Ser							
			545														550				555	
tgg	tcc	aaa	acc	tat	gaa	aat	gtt	gaa	ttt	gaa	acc	acc	tct	ttt	acc	1731						
Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr							
			560														565				570	
ttc	tcc	tat	att	gcc	caa	gaa	tga	aaaagcggcc	gctc	gagtct	agagggccccg						1785					
Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*															
			575														580					
tttaaacccg	ctgatcagcc	tcgactgtgc	cttctagttg	ccagccatct	gttg	tttgcc	1845															
cctcccccg	gccttccttg	ancctggaan	gtgccactcc	cactgtcctt	tcctaataaa	1905																
atgaggaaat	gcac															1920						
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<211> 580																						
<212> PRT																						
<213> Artificial Sequence																						
<220>																						
<223> Ad5s/Ad37k																						
<400> 53																						
Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro							
1				5					10					15								
Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro							
			20					25					30									
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser							
			35				40					45										
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu							
	50					55					60											
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser							
65					70					75					80							
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn							
			85						90					95								
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu							
			100					105					110									
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr							
			115				120					125										
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile							
			130			135					140											
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln							
145					150					155					160							
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr							
				165					170					175								
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu							
			180					185					190									
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly							
		195					200					205										
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr							
					215						220											
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr							
225					230					235					240							
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln															

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290		295		300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu				
305		310		315
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile				
		325		330
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro				
		340		345
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp				
		355		360
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp				
		370		375
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr				
		385		390
Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp				
		405		410
Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile				
		420		425
Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile				
		435		440
Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu				
		450		455
Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala				
		465		470
Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu				
		485		490
Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser				
		500		505
Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu				
		515		520
Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln				
		530		535
Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys				
		545		550
Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr				
		565		570
Ile Ala Gln Glu				575
		580		

<210> 54
 <211> 1767
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s fiber

<221> CDS
 <222> (13)...(1749)

<400> 54
 atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly

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30	35	40	45	
gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg	195			
Val Leu Ser Leu Arg 50	Leu Ser Glu Pro Leu 55	Val Thr Ser Asn Gly 60	Met	
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc gcc agc	243			
Leu Ala Leu Lys 65	Met Gly Asn Gly 70	Leu Ser Leu Asp Glu Ala Gly 75	Ser	
cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac	291			
Leu Thr Val Asn 80	Pro Lys Ala Pro 85	Leu Gln Val Asn Thr 90	Asp Ser Asn	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	339			
Ile Asn Leu Glu 95	Ile Ser Ala Pro 100	Leu Thr Val Thr 105	Ser Glu Ala Leu	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	387			
Thr Val Ala Ala 110	Ala Ala Pro Leu 115	Met Val Ala Gly 120	Asn Thr Leu Thr 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	435			
Met Gln Ser Gln 130	Ala Pro Leu Thr 135	Val His Asp Ser 140	Lys Leu Ser Ile 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	483			
Ala Thr Gln Gly 145	Pro Leu Thr Val 150	Ser Glu Gly Lys Leu 155	Ala Leu Gln	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	531			
Thr Ser Gly Pro 160	Leu Thr Thr 165	Asp Ser Ser Thr 170	Leu Thr Ile Thr	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	579			
Ala Ser Pro Pro 175	Leu Thr Thr 180	Ala Thr Gly Ser 185	Leu Gly Ile Asp Leu	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	627			
Lys Glu Pro Ile Tyr 190	Thr Gln Asn Gly 195	Lys Leu Gly Leu 200	Lys Tyr Gly 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	675			
Ala Pro Leu His 210	Val Thr Asp Asp 215	Leu Asn Thr Leu 220	Val Ala Thr 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	723			
Gly Pro Gly Val 225	Thr Ile Asn Asn 230	Ser Leu Gln Thr 235	Lys Val Thr	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	771			
Gly Ala Leu Gly 240	Phe Asp Ser Gln 245	Gly Asn Met Gln 250	Leu Asn Val Ala	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	819			
Gly Gly Leu Arg 255	Ile Asp Ser Gln 260	Asn Arg Arg Leu 265	Ile Leu Asp Val	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	867			
Ser Tyr Pro Phe Asp 270	Ala Ala Gln Asn 275	Gln Leu Asn Leu 280	Arg Leu Gly Gln 285	

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ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	915
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	963
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
305 310 315	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1011
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
320 325 330	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1059
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
335 340 345	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1107
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
350 355 360 365	
tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac	1155
Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp	
370 375 380	
aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1203
Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr	
385 390 395	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	1251
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
400 405 410	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1299
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
415 420 425	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1347
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
430 435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1395
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
450 455 460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	1443
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe	
465 470 475	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga	1491
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly	
480 485 490	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	1539
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
495 500 505	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	1587
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
510 515 520 525	

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cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
      530      535      540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
      545      550      555

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
      560      565      570

tac att gcc caa gaa taa agaagcggcc gcgttatg 1767
Tyr Ile Ala Gln Glu *
      575

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<210> 55
 <211> 578
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s

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<400> 55
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1      5      10      15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
      20      25      30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
      35      40      45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
      50      55      60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val
      65      70      75      80
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu
      85      90      95
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala
      100      105      110
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser
      115      120      125
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln
      130      135      140
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly
      145      150      155      160
Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro
      165      170      175
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro
      180      185      190
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu
      195      200      205
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly
      210      215      220
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu
      225      230      235      240
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu
      245      250      255
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro
      260      265      270
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu

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[illegible]

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<210> 56
<211> 1132
<212> DNA
<213> Artificial Sequence
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<220>
<223> Ad37s/Ad5k fiber

```
<221> CDS
<222> (16) ... (1116)
```

```
<221> misc_feature
<222> 1125
<223> n = A,T,C or G
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<400> 56
gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
1 5 10

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ccc gtc tac ccc tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc 99
 Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu
 15 20 25

act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly
 30 35 40

gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat 195
 Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp
 45 50 55 60

gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta 243
 Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu
 65 70 75

act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt 291
 Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu
 80 85 90

gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt 339
 Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser
 95 100 105

tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg 387
 Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala
 110 115 120

ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga 435
 Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly
 125 130 135 140

ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att 483
 Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile
 145 150 155

ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga 531
 Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
 160 165 170

tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc 579
 Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr
 175 180 185

aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct 627
 Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
 190 195 200

aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca 675
 Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
 205 210 215 220

gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca 723
 Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
 225 230 235

gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta 771
 Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
 240 245 250

cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga 819

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```

Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
    255                260                265
gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct 867
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
    270                275                280

aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac 915
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
    285                290                295                300

att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca 963
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
    305                310                315

cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca 1011
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
    320                325                330

agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac 1059
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
    335                340                345

att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc 1107
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
    350                355                360

caa gaa taa agaagcggnc gctcga 1132
Gln Glu *
365

```

<210> 57
 <211> 366
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k

```

<400> 57
Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1      5      10      15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20      25      30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35      40      45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50      55      60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65      70      75      80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85      90      95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
100      105      110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
115      120      125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
130      135      140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145      150      155      160

```

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```

Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
      165      170
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Ala Pro
      180      185
Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu
      195      200      205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu
      210      215      220
Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala
      225      230      235
His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser
      245      250      255
Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu
      260      265      270
Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala
      275      280      285
Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln
      290      295      300
Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr
      305      310      315
Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser
      325      330      335
Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile
      340      345      350
Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
      355      360      365

```

<210> 58
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37 third repeat

```

<400> 58
Gly Ser Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp
 1           5           10           15

```

<210> 59
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad8 last repeat

```

<400> 59
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
 1           5           10

```

<210> 60
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad9 last repeat

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<400> 60
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asn Asp .
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 last repeat

<400> 61
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala
1 5 10

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton region

<400> 62
His Ala Ile Arg Gly Asp Thr Phe
1 5

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
1 5 10 15

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
1

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

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<220>
 <223> HSP binding motif

<400> 65
 Lys Lys Thr Lys
 1

<210> 66
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad8 third repeat

<400> 66
 Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
 1 5 10 15

<210> 67
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad9 third repeat

<400> 67
 Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
 1 5 10 15

<210> 68
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad15 third repeat

<400> 68
 Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
 1 5 10 15

<210> 69
 <211> 3929
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector pCR2.1

<400> 69
 agcgcccaat acgcaaaccg cctctccccg cgcgttgcc gattcattaa tgcagctggc 60
 acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
 tcaactatta ggcaccccag gctttacact ttatgcttcc ggctcgatg ttgtgtggaa 180
 ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
 gtaccgagct cggatccact agtaacggcc gccagtgtgc tgggaattcgg ctttaagccga 300

attctgcaga	tatccatcac	actggcgggc	gctcgagcat	gcactctagag	ggcccaattc	360
gccctatagt	gagtcgtatt	acaattcact	ggcgcgtcgtt	ttacaacgtc	gtgactggga	420
aaaccctggc	gttaccacaac	ttaatcgctt	tgcagcacat	ccccctttcg	ccagctggcg	480
taatagcgaa	gagggccgca	ccgatcgccc	ttcccaacag	ttgcgcagcc	tgaatggcga	540
atggacgcgc	cctgtagcgg	cgcattaagc	gcggcggttg	tgggtggttac	gcgcagcgtg	600
accgctacac	ttgccagcgc	cctagcgccc	gctcctttcg	ctttcttccc	ttcctttctc	660
gccacgttcg	ccggttttcc	ccgtcaagct	ctaaatcggtg	ggctcccttt	agggttccga	720
tttagtgctt	tacggcacct	cgaccccaaa	aaacttgatt	aggggtgatgg	ttcacgtagt	780
gggccatcgc	cctgatagac	ggttttttcg	cctttgacgt	tggagtccac	gttctttaat	840
agtggactct	tgttccaaac	tggaaacaaca	ctcaacccta	tctcgttcta	ttcttttgat	900
ttataaggga	ttttgccgat	ttcggcctat	tgggttaaaaa	atgagctgat	ttaacaaaaa	960
tttaacgcga	attttaacaa	aatttcagggc	gcaagggctg	ctaaagggaag	cggaaacacgt	1020
agaaagccag	ttccgcagaaa	cgggtgctgac	cccggatgaa	tgtcagctac	tgggctatct	1080
ggacaaggga	aaagcgaagc	gcaaagagaa	agcaggtagc	ttgcagtggg	cttacatggc	1140
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cctctggtaa	ggttgggaag	ccctgcaaa	taaactggat	ggctttcttg	ccgccaagga	1260
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atgactgggc	acaacagaca	atcggctgct	ctgatgccgc	cgtgttccgg	ctgtcagcgc	1440
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taaccgtatt	accgcctttg	agttagctga	taccgctcgc	cgcagccgaa	cgaccgagcg	3900
cagcgagtca	gtgagcgagg	aagcggaag				3929

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<210> 70
 <211> 3931
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector pCR2.1-Topo

<400> 70
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 acgacagggt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagtttagc 120
 tcaactcatta ggcacccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
 ttgtgagcgg ataacaatth cacaaggaa acagctatga ccatgattac gccaaagcttg 240
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 gaattctgca gatataccatc aactggcggg ccgctcgagc atgcatctag agggcccaat 360
 tcgcccataa gtgagtcgta ttacaattca ctggccgctcg ttttacaacg tcgtgactgg 420
 gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt cgccagctgg 480
 cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag cctgaatggc 540
 gaatggacgc gccctgtagc ggcgcatata gcgcggcggg tgtgggtgggt acgcgcagcg 600
 tgaccgctac actttgcagc gccctagcgc ccgctccttt cgctttcttc ccttcctttc 660
 tcgcccagctt cgcgggcttt ccccgtaaac ctctaaatcg ggggctccct ttaggggttc 720
 gatttagtgc tttacggcac ctgcacccca aaaaacttga ttaggggtgat ggttcacgta 780
 gtgggcccac gccctgatag acggtttttc gccctttgac gttggagtcc acgttcttta 840
 atagtggact cttgttccaa actggaacaa cactcaaccc tatctcggtc tattcttttg 900
 atttataagg gattttgccg atttcggcct attgggttaa aaatgagctg atttaacaaa 960
 aatttaacgc gaattttaac aaaattcagg gcgcaagggg tgctaaagga agcgggaacac 1020
 gtagaaagcc agtccgcaga aacgggtgctg accccggatg aatgtcagct actgggctat 1080
 ctggacaagg gaaaacgcaa gcgcaagagag gcttgcaagt gcttgcaagt ggcttacatg 1140
 gcgatagcta gactgggccc agccctgcaa agcaaacgaa ccggaattgc cagctggggc 1200
 gccctctggg aagggttggg agccctgcaa agtaaaactg atggctttct tgccgccaag 1260
 gatctgatgg cgcaggggat caagatctga tcaagagaca ggatgaggat cgtttcgcat 1320
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 caagtttact catatatact ttagattgat ttaaaacttc atttttaatt taaaaggatc 3060

-51-

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cgcgtaatct	gctgcttgca	aacaaaaaaaa	ccaccgctac	cagcgggtgg	ttgtttgccc	3240
gatcaagagc	taccaactct	ttttccgaag	gtaactggct	tcagcagagc	gcagatacca	3300
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